#2

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RAW SEQUENCE LISTING   DATE: 01/25/2002
PATENT APPLICATION: US/09/808,885   TIME: 17:00:10

Input Set : **N:\Crf3\RULE60\09808885.raw**
Output Set: **N:\CRF3\01252002\I808885.raw**

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: Hillman, Jennifer
 6                      Corley, Neil C.
 7                      Shah, Purvi
 9      (ii) TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
11     (iii) NUMBER OF SEQUENCES: 3
13      (iv) CORRESPONDENCE ADDRESS:
14           (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15           (B) STREET: 3174 Porter Drive
16           (C) CITY: Palo Alto
17           (D) STATE: CA
18           (E) COUNTRY: USA
19           (F) ZIP: 94304
21       (v) COMPUTER READABLE FORM:
22           (A) MEDIUM TYPE: Diskette
23           (B) COMPUTER: IBM Compatible
24           (C) OPERATING SYSTEM: DOS
25           (D) SOFTWARE: FastSEQ for Windows Version 2.0
27      (vi) CURRENT APPLICATION DATA:
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C--> 28   **(A) APPLICATION NUMBER: US/09/808,885**
C--> 29   **(B) FILING DATE: 14-Mar-2001**
```
30           (C) CLASSIFICATION:
32     (vii) PRIOR APPLICATION DATA:
33           (A) APPLICATION NUMBER: 09/295,055
34           (B) FILING DATE:
36    (viii) ATTORNEY/AGENT INFORMATION:
37           (A) NAME: Billings, Lucy J.
38           (B) REGISTRATION NUMBER: 36,749
39           (C) REFERENCE/DOCKET NUMBER: PF-0354 US
41      (ix) TELECOMMUNICATION INFORMATION:
42           (A) TELEPHONE: 415-855-0555
43           (B) TELEFAX: 415-845-4166
44           (C) TELEX:
47 (2) INFORMATION FOR SEQ ID NO: 1:
49       (i) SEQUENCE CHARACTERISTICS:
50           (A) LENGTH: 290 amino acids
51           (B) TYPE: amino acid
52           (C) STRANDEDNESS: single
53           (D) TOPOLOGY: linear
55     (vii) IMMEDIATE SOURCE:
56           (A) LIBRARY: PROSNON01
57           (B) CLONE: 2272281
```

ENTERED

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59      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61   Met Lys Arg Asn Ser Pro Gln Lys Ile Lys Lys Arg Lys Asp Arg Arg
62    1               5                   10                  15
63   Ala Lys Lys Gln Ser Phe Asp Asp Asn Asp Ser Glu Glu Leu Glu Asp
64               20              25              30
65   Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys Pro Lys Val Glu Met Tyr
66           35              40              45
67   Ser Gly Ser Asp Asp Asp Asp Phe Asn Lys Leu Pro Lys Lys Ala
68       50              55              60
69   Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys Trp Asp Gly Ser Glu Glu
70    65              70              75                  80
71   Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu Arg Ser Arg Ile Asn Ser
72                   85              90                  95
73   Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu Phe Leu Gln Ser Arg Lys
74               100             105             110
75   Gly Gln Lys Lys Asn Gln Lys Asn Lys Pro Gly Pro Asn Ile Glu Ser
76           115             120             125
77   Gly Asn Glu Asp Asp Asp Ala Ser Phe Lys Ile Lys Thr Val Ala Gln
78       130             135             140
79   Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg Asp Glu Glu
80    145             150             155                 160
81   Lys Ala Lys Leu Arg Lys Leu Lys Glu Lys Glu Glu Leu Glu Thr Gly
82               165             170             175
83   Lys Lys Asp Gln Ser Lys Gln Lys Glu Ser Gln Arg Lys Phe Glu Glu
84               180             185             190
85   Glu Thr Val Lys Ser Lys Val Thr Val Asp Thr Gly Val Ile Pro Ala
86           195             200             205
87.  Ser Glu Glu Lys Ala Glu Thr Pro Thr Ala Ala Glu Asp Asp Asn Glu
88       210             215             220
89   Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Gly Glu Lys Glu
90    225             230             235                 240
91   Glu Lys Glu Lys Glu Lys Lys Lys Gly Pro Ser Lys Ala Thr Val Lys
92               245             250             255
93   Ala Met Gln Glu Ala Leu Ala Lys Leu Lys Glu Glu Glu Glu Arg Gln
94               260             265             270
95   Lys Arg Glu Glu Glu Glu Arg Ile Lys Arg Leu Glu Glu Leu Glu Ser
96           275             280             285
97   Lys Pro
98       290
100 (2) INFORMATION FOR SEQ ID NO: 2:
102      (i) SEQUENCE CHARACTERISTICS:
103          (A) LENGTH: 1434 base pairs
104          (B) TYPE: nucleic acid
105          (C) STRANDEDNESS: single
106          (D) TOPOLOGY: linear
108     (vii) IMMEDIATE SOURCE:
109          (A) LIBRARY: PROSNON01
110          (B) CLONE: 2272281
112      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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RAW SEQUENCE LISTING   DATE: 01/25/2002
PATENT APPLICATION: US/09/808,885   TIME: 17:00:10

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114  CTGTTCCAGT GCGCGGGTCT GTGGAGAGCC GGGTGCGAGC GGCGGCAGCA CGAGGGGAAA     60
115  AGAGCTGAGC GGAGACCAAA GTCAGCCGGG AGACAGTGGG TCTGTGAGAG ACCGAATAGA    120
116  GGGGCTGGGG CCACGAGCGC CATTGACAAG CAATGGGGAA GAAACAGAAA AACAAGAGCG    180
117  AAGACAGCAC CAAGGATGAC ATTGATCTTG ATGCCTTGGC TGCAGAAATA GAAGGAGCTG    240
118  GTGCTGCCAA AGAACAGGAG CCTCAAAAGT CAAAAGGGAA AAAGAAAAAA GAGAAAAAAA    300
119  AGCAGGACTT TGATGAAGAT GATATCCTGA AAGAACTGGA AGAATTGTCT TTGGAAGCTC    360
120  AAGGCATCAA AGCTGACAGA GAAACTGTTG CAGTGAAGCC AACAGAAAAC AATGAAGAGG    420
121  AATTCACCTC AAAAGATAAA AAAAGAAAG GACAGAAGGG CAAAAAAACA GAGTTTTGAT    480
122  GATAATGATA GCGAAGAATT GGAAGATAAA GATTCAAAAT CAAAAAAGAC TGCAAAACCG    540
123  AAAGTGGAAA TGTACTCTGG GAGTGATGAT GATGATGATT TTAACAAACT TCCTAAAAAA    600
124  GCTAAAGGGA AAGCTCAAAA ATCAAATAAG AAGTGGGATG GGTCAGAGGA GGATGAGGAT    660
125  AACAGTAAAA AAATTAAAGA GCGTTCAAGA ATAAATTCTT CTGGTGAAAG TGGTGATGAA    720
126  TCAGATGAAT TTTTGCAATC TAGAAAAGGA CAGAAAAAAA ATCAGAAAAA CAAGCCAGGT    780
127  CCTAACATAG AAAGTGGGAA TGAAGATGAT GACGCCTCCT TCAAAATTAA GACAGTGGCC    840
128  CAAAAGAAGG CAGAAAAGAA GGAGCGCGAG AGAAAAAAGC GAGATGAAGA AAAAGCGAAA    900
129  CTGCGGAAGC TGAAAGAAAA AGAAGAGTTA GAAACAGGTA AAAAGGATCA GAGTAAACAA    960
130  AAGGAATCTC AAAGGAAATT TGAAGAAGAA ACTGTAAAAT CCAAAGTGAC TGTTGATACT   1020
131  GGAGTAATTC CTGCCTCTGA AGAGAAAGCA GAGACTCCCA CAGCTGCAGA AGATGACAAT   1080
132  GAAGGAGACA AAAAGAAGAA AGATAAGAAG AAAAAGAAAG GAGAAAAGGA AGAAAAAGAG   1140
133  AAAGAGAAGA AAAAAGGACC TAGCAAAGCC ACTGTTAAAG CTATGCAAGA AGCTCTGGCT   1200
134  AAGCTTAAAG AGGAAGAAGA AAGACAGAAG AGAGAAGAGG AAGAACGTAT AAAACGGCTT   1260
135  GAAGAATTAG AAAGCAAGCC GTAAGCACAA GGAACCGTTT GGAACCCAGA CCAAAAGAGC   1320
136  AAGGGCACAG GCAAGACACC AAACCAAGGG GCGGCCCCCG AATTAATGTA CCTCTTCGCA   1380
137  CCGGGACTTC CTTTCGGGGC CGTTCCTGCA AGCGGAACCA ATTTTCCCTA AAGG         1434
139  (2) INFORMATION FOR SEQ ID NO: 3:
141        (i) SEQUENCE CHARACTERISTICS:
142             (A) LENGTH: 234 amino acids
143             (B) TYPE: amino acid
144             (C) STRANDEDNESS: single
145             (D) TOPOLOGY: linear
147       (vii) IMMEDIATE SOURCE:
148             (A) LIBRARY: GenBank
149             (B) CLONE: 1514949
151       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
153  Gly Gln Lys Gly Lys Lys Thr Ser Phe Asp Glu Asn Asp Ser Glu Glu
154    1               5                  10                  15
155  Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Pro Ala Arg Pro Asn Ser
156             20                  25                  30
157  Glu Val Leu Leu Ser Gly Ser Glu Asp Ala Asp Asp Pro Asn Lys Leu
158             35                  40                  45
159  Ser Lys Lys Gly Lys Lys Ala Gln Lys Ser Thr Lys Lys Arg Asp Gly
160        50                  55                  60
161  Ser Glu Glu Asp Glu Asp Asn Ser Lys Arg Ser Lys Glu Arg Ser Arg
162  65                  70                  75                  80
163  Val Asn Ser Ser Gly Glu Ser Gly Gly Glu Ser Asp Glu Phe Leu Gln
164             85                  90                  95
165  Ser Arg Lys Gly Gln Lys Lys Asn Gln Lys Asn Lys Ser Val Pro Thr
166             100                 105                 110
167  Ile Asp Ser Gly Asn Glu Asp Asp Asp Ser Ser Phe Lys Ile Lys Thr
```

```
168              115                   120                   125
169   Val Ala Gln Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg
170         130              135                   140
171   Glu Glu Glu Lys Ala Lys Leu Arg Lys Val Lys Glu Lys Glu Glu Leu
172   145                   150                   155                   160
173   Glu Lys Gly Arg Lys Glu Gln Ser Lys Gln Arg Glu Pro Gln Lys Arg
174                     165                   170                   175
175   Pro Asp Glu Glu Val Leu Val Leu Arg Gly Thr Pro Asp Ala Gly Ala
176             180          185                   190
177   Ala Ser Glu Glu Lys Gly Asp Ile Ala Ala Thr Leu Glu Asp Asp Asn
178         195              200                   205
179   Glu Gly Asp Lys Lys Lys Lys Asp Lys Lys Lys Lys Lys Thr Glu Lys
180         210              215                   220
181   Asp Asp Lys Glu Lys Glu Lys Lys Lys Gly
182   225              230
```

VERIFICATION SUMMARY   DATE: 01/25/2002
PATENT APPLICATION: US/09/808,885   TIME: 17:00:11

Input Set : N:\Crf3\RULE60\09808885.raw
Output Set: N:\CRF3\01252002\I808885.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]